

Figure 1

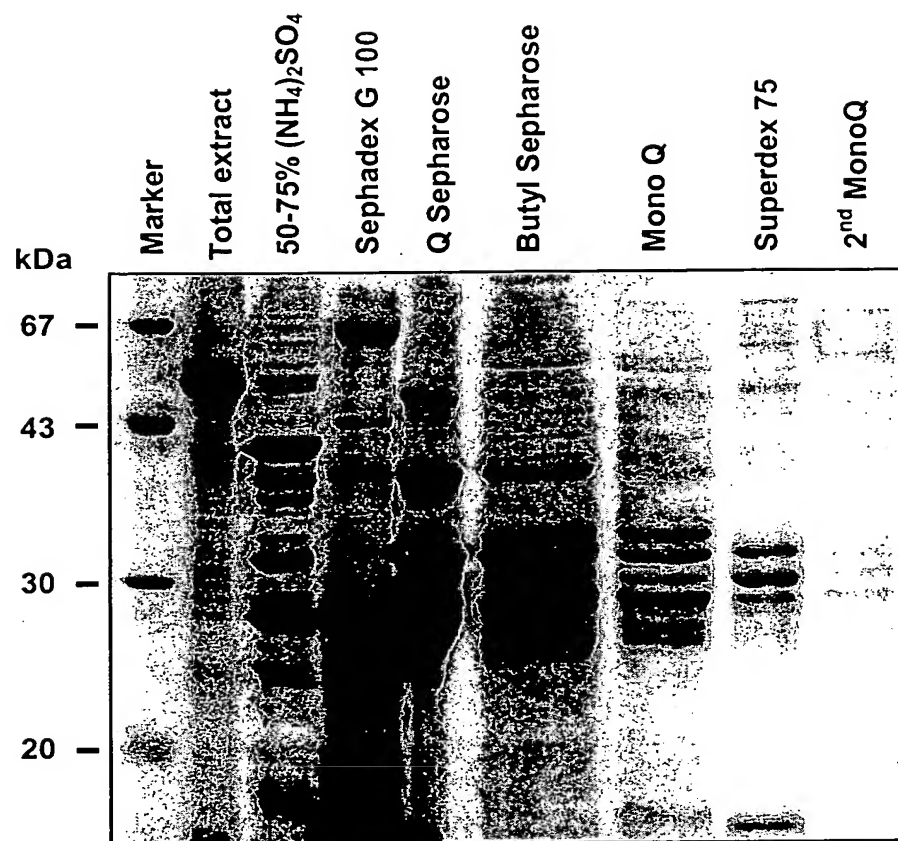


Figure 2

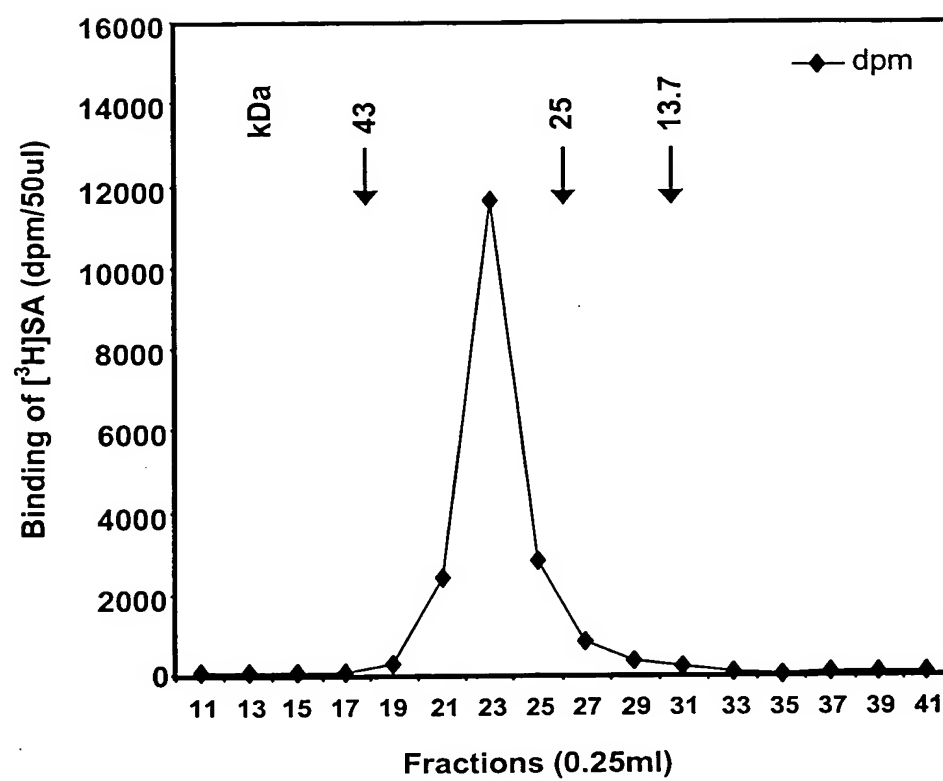
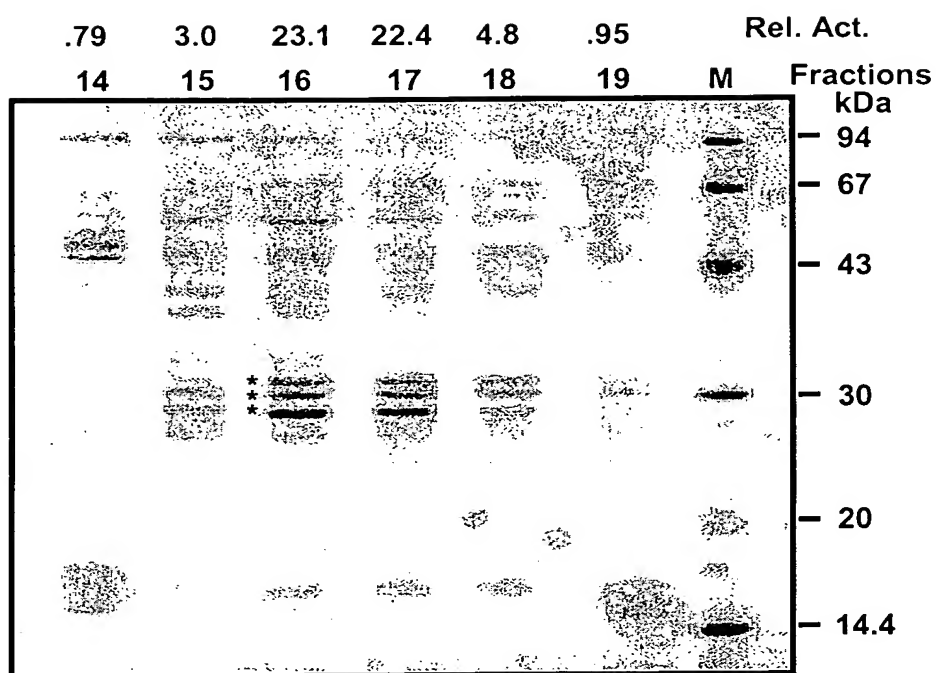


Figure 3



1	acgcggggaagaaactaacaggcataataattcaa	ATG AAG GAA GGA AAA CAC TTT GTT TTA GTA CAT GGT GCA TGC	83
1	M K E G K H F V L V H G A C		14
84	CAT GGA GGT TGG AGT TGG TAC AAG CTA AAG CCA CTG CTA GAA GCT GCA GGC CAT AAG GTT ACA GCC CTT GAT TTA	158	
15	H G G W S W Y K L K P L L E A A G H K V T A L D L	39	
159	GCA GCT TCT GGC ACT GAT TTG AGA AAA ATA GAG GAG CTT CGC ACA CTT TAT GAT TAT ACT TTG CCA TTG ATG GAG	233	
40	A A S G T D L R K I E E L R T L Y D Y T L P L M E	64	
	<u>peptide # 1 (pk22a, pk23 &amp; pk55*)</u>		
234	TTG ATG GAA TCT CTT TCA GCA GAT GAG AAG GTT ATA TTA GTG GGG CAT AGT CTT GGT GGT ATG AAT TTG GGA CTT	308	
65	L M E S L S A D E K V I L V G H S L G G M N L G L	89	
309	GCT ATG GAA AAG TAT CCA CAA AAG ATC TAT GCT GCT TTC GCT GCT TTC ATG CCT GAT TCT GTT CAC AAC	383	
90	A M E K Y P Q K I Y A A V F L A A F M P D S V H N	114	
384	TCC TCC TTT GTT TTG GAA CAG TAT AAT GAG CGG ACG CCA GCC GAG AAT TGG TTG GAT ACT CAG TTT TTA CCA TAT	458	
115	S S F V L E Q Y N E R T P A E N W L D T Q F L P Y	139	
459	GGT TCC CCT GAA GAG CCA CTG ACA TCC ATG TTT TTT GGC CCA AAG TTC TTG GCT CAC AAG CTC TAC CAG CTA TGC	533	
140	G S P E E P L T S M F F G P K F L A H K L Y Q L C	164	
	<u>peptide # 3 (pk29)</u>		
534	TCT CCT GAG GAT CTT GCA TTA GCA TCA TCA TTG GTG AGA CCA AGC TCT TTG TTT ATG GAA GAC CTA TCG AAG GCC	608	
165	S P E D L A L A S S L V R P S S L F M E D L S K A	189	
609	AAG TAT TTC ACA GAT GAA CGG TTT GGA TCA GTG AAG AGA GTT TAC ATT GTG TGC ACT GAG GAT AAA GGC ATA CCA	683	
190	K Y F T D E R F G S V K R V Y I V C T E D K G I P	214	
	<u>peptide # 5 (pk30 &amp; pkx)</u>		
684	GAA GAA TTC CAG CGA TGG CAA ATT GAC AAC ATT GGT GTC ACT GAA GCA ATA GAG ATT AAA GGT GCT GAT CAC	758	
215	E E F Q R W Q I D N I G V T E A I E I K G A D H M	239	
759	GCA ATG CTA TGC GAG CCC CAA AAA CTT TGC GCC TCT CTC TTG GAA ATT GCC CAT AAA TAC AAC TGA tctctacatt	834	
240	A M L C E P Q K L C A S L L E I A H K Y N *	261	
837	atgtcttcgtcatgtcaagattttcagtgcatgtctaatttttctatttttcgaaccggcgcaataactgtctttgccatttttaaggatttcagt	933	
937	aatttcactcttagtggaaggtccacataaaggattgttctgttttccattccaagtggttatgttgagatacttaaacgatatcaattct	1032	
1037	tgtaatgaaaacttcttcttcttcttbtgaaaaaiaaaaaaaaaaaaaa	1079	

SABP2-*N. tabacum* MKEGK-----HFVLVHGACHGGWSWYKLPLLEAAGHKVTALDLAASGTD-LRKIEELRTL 55  
*A. thaliana* MSECKR-KQHFVLVHGSCHGAWCWYKVPLLEAVGHRVTAVDLAASGITDTRTSITDIPTC 59  
*M. esculenta* MAVDV-----FVLIIHTICHGAWIWKLPVLEAAGHKVTALDLAASGDV-PRQIEQINSF 54  
*H. brasiliensis* MAFAH-----FVLIHTICHGAWIWHKLPLLEALGHKVTALDLAASGVDP-PROJEEIGSF 54  
PIR7B MEISSSSKKHFIILVHGLCHGAWCWYRVVAALRAAGHRATALDMAASGAH-PARVDEVGTF 59  
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SABP2-*N. tabacum* YDYTLPLMELMESLSA-DEKVLIVGSHLGSSMNLGLAMEKYPKIYA AVFLAAFPDPSVHN 114  
*A. thaliana* EQYSEPLTKLLTSLPN-DEKVVLVGHSGCGGLNIAIMEKFPKISAVAVFLTAFMPDTEHS 118  
*M. esculenta* DEYSEPLLTFMESLPQ-GEKVLIVGESCGGLNIAIAADKYCEKIAAAVFQNSSLPDTHKH 113  
*H. brasiliensis* DEYSEPLLTFLEALPP-GEKVLIVGESCGGLNIAIAADKYCEKIAAAVFHNSVLPDTEHC 113  
PIR7B EYSRPLLDVA AAAAAPGERLVLVGHSHGGLSVALAMERFPDKVAAA VFVAAAMPVCVGKH 119  
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SABP2-*N. tabacum* SSFVLEQYN-ERTPAENWLDTQFLPYGS-PEEPLTSMFFGPKFLAHKLYQLCSPEDLALA 172  
*A. thaliana* PSFVLDFKG-SNMPPQEAWMGTETEPFGYS-DNSGLS-MFFSPDFMKGLYLQSPVEDLELG 175  
*M. esculenta* PSYVVDKLM-EVFP--DWKDTEYFEFSNSNGETITGMVLGLKMRENLYTICPPDEYELA 170  
*H. brasiliensis* PSYVVDKLM-EVFP--DWKDDTYFTYT/K-DGKEITGLKLGFTLLRENLYTLCGPPEYE LA 169  
PIR7B MGVPTEEFMRRTAPEGLLMDCEMVA INNSQGSGVA-INLGPTFLAQKYQQSPAEDLALA 178  
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SABP2-*N. tabacum* SSLVRPSSLFMEDLSKAK--YFTDERFGSVKRYVI VCTEDKGIP EEFQRWQIDNIGVTEA 230  
*A. thaliana* LLLMRPGSLFINDSLKMK--NFSDGYGVSVP RVFICKEDKA IPEERQRWMIDNFPNVLV 238  
*M. esculenta* KMLTRRGSLFWQSILA QRE--KFTEGYGSIKKIYVWTGDDKIFLPEFQLWQIENYKPD LV 223  
*H. brasiliensis* KMLTRKGS LFQNILAKRP--FFTKEGYGSIKKIYVWTDQDEIFLPEFQLWQIENYKPKDV 227  
PIR7B KMLVRPGNQFMDDPVMKDES LLTNGNYG SVKKYVVI AKADSSTEEMQRWVMAMSPGTDV 238  
\* \* . \* . :.: \*\*: :.: \* . \* \* \* :

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SABP2-*N. tabacum* IEIKGADHMAMLCEPQKLCASLLEIAHKVN 260  
*A. thaliana* MEMEETHDMPMFCFKPQQLSDYFLKIADKFV 263  
*M. esculenta* FRVMGGDHKLQLTKTNEIAGILQKVADIYA 258  
*H. brasiliensis* YKVEGGDHKLQLTKTKEIAEILQEVA DTYN 257  
PIR7B EEIAGADHAVMSKPRELCDILIKIAN KY 268  
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Fig. 6A



Fig. 6B

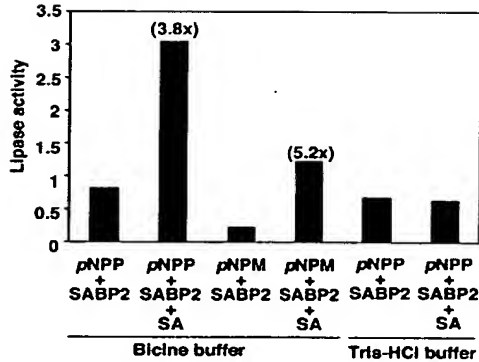


Fig. 7A

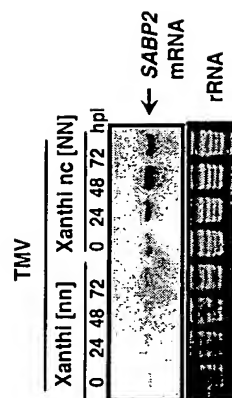
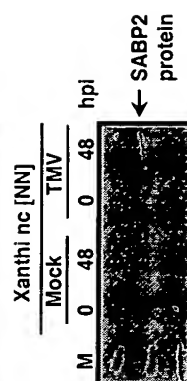


Fig. 7B



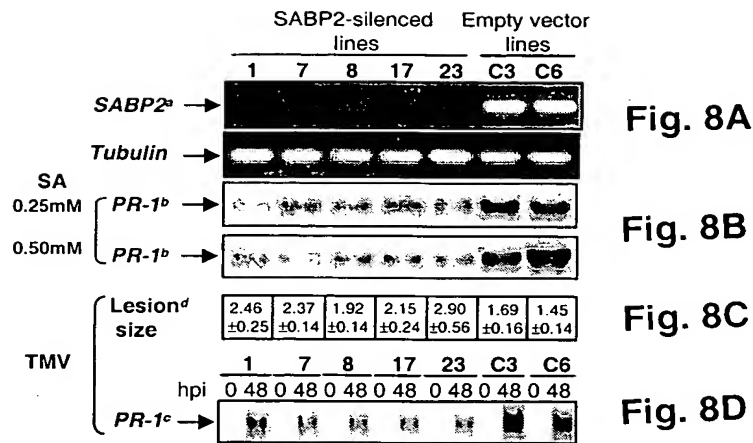


Fig. 8E

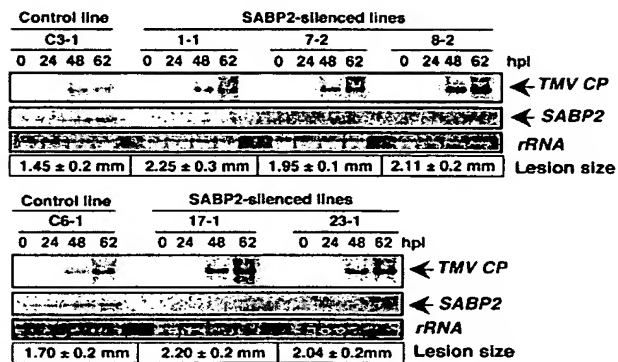


Fig. 8F

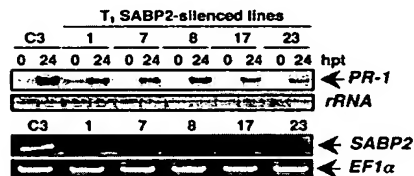


Fig. 8G

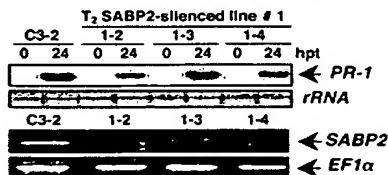




Fig. 9A

Lines	TMV lesion size $\pm$ SD (mm)		SAR
	Primary Infection	Secondary Infection	
Control	1.71 $\pm$ 0.19	0.85 $\pm$ 0.25	yes
SABP2-silenced	2.08 $\pm$ 0.12	2.19 $\pm$ 0.31	no

Fig. 9B

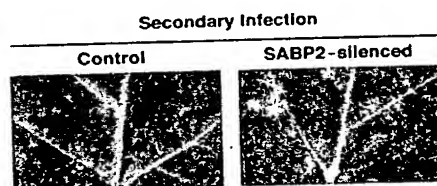
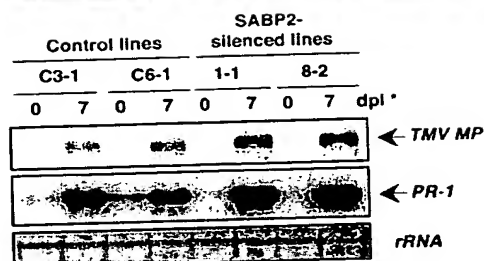
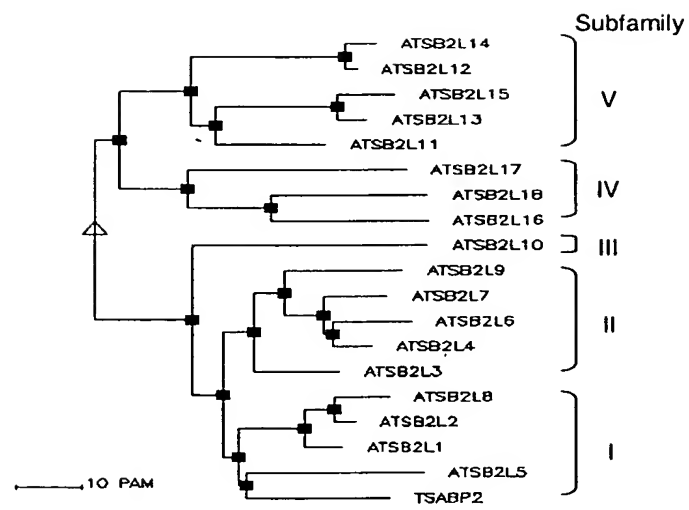


Fig. 9C





**Figure 10**